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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/487,283ADATE: 03/24/97
TIME: 17:17:25

INPUT SET: S16458.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
23 (1) General Information:
4

5 (i) APPLICANT: Evans, Mark J.
6 Matis, Louis A.
7 Mueller, Eileen Elliott
8 Nye, Steven H.
9 Rollins, Scott
10 Rother, Russell P.
11 Springhorn, Jeremy P.
12 Squinto, Stephen P.
13 Thomas, Thomas C.
14 Wilkins, James A.
15

16 (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT
17 OF INFLAMMATORY DISEASES

18 (iii) NUMBER OF SEQUENCES: 26

19 (iv) CORRESPONDENCE ADDRESS:

20 (A) ADDRESSEE: Seth A. Fidel
21 (B) STREET: 25 Science Park (Alexion)
22 (C) CITY: New Haven
23 (D) STATE: Connecticut
24 (E) COUNTRY: USA
25 (F) ZIP: 06511

26 (v) COMPUTER READABLE FORM:

27 (A) MEDIUM TYPE: 3.5 inch, 1.4Mb storage
28 (B) COMPUTER: Macintosh Cetris 610

29 (C) OPERATING SYSTEM: System 7

30 (D) SOFTWARE: WordPerfect 3.0

31 (vi) CURRENT APPLICATION DATA:

32 (A) APPLICATION NUMBER: 08/487,283

33 (B) FILING DATE: June 7, 1995

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US 08/236,208

36 (B) FILING DATE: 02-MAY-1994

37

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Seth A. Fidel.

40 (B) REGISTRATION NUMBER: 38,449

41 (C) REFERENCE/DOCKET NUMBER: ALX-152.1 CIP

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: (203)776-1790

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5/2
B. Derry
1/23/97

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47 (B) TELEFAX: (203)772-3655
48
49
50
51 (2) INFORMATION FOR SEQ ID NO:1:
52 (i) SEQUENCE CHARACTERISTICS:
53 (A) LENGTH: 21 amino acids
54 (B) TYPE: Amino Acid
55 (C) STRANDEDNESS: Single
56 (D) TOPOLOGY: Linear
57 (ii) MOLECULE TYPE:
58 (A) DESCRIPTION: KSSKC peptide
59 (iii) HYPOTHETICAL: No
60 (iv) ANTI-SENSE: No
61
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64 Val Ile Asp His Gln Gly Thr Lys Ser Ser
65 5 10
66
67 Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser
68 15 20
69
70
71 (2) INFORMATION FOR SEQ ID NO:2:
72 (i) SEQUENCE CHARACTERISTICS:
73 (A) LENGTH: 1676 Amino Acids
74 (B) TYPE: Amino Acid
75 (C) STRANDEDNESS: Single
76 (D) TOPOLOGY: Linear
77 (ii) MOLECULE TYPE:
78 (A) DESCRIPTION: Pro-C5 Polypeptide
79 (iii) HYPOTHETICAL: No
80 (iv) ANTI-SENSE: No
81 (vi) ORIGINAL SOURCE:
82 (A) ORGANISM: Homo sapiens
83 (x) PUBLICATION INFORMATION:
84 (A) AUTHORS: Haviland, D.L.
85 Haviland, J.C.
86 Fleischer, D.T.
87 Hunt, A.
88 Wetsel, R.A.
89
90 (B) TITLE: Complete cDNA Sequence of Human
91 Complement Pro-C5
92 (C) JOURNAL: Journal of Immunology
93 (D) VOLUME: 146
94 (F) PAGES: 362-368
95 (G) DATE: 1991
96
97
98 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
99

RAW SEQUENCE LISTING
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100 Met Gly Leu Leu Gly Ile Leu Cys Phe Leu
101 -15 -10
102
103 Ile Phe Leu Gly Lys Thr Trp Gly Gln Glu Gln Thr Tyr Val
104 -5 -1 5
105
106 Ile Ser Ala Pro Lys Ile Phe Arg Val Gly Ala Ser Glu Asn
107 10 15 20
108
109 Ile Val Ile Gln Val Tyr Gly Tyr Thr Glu Ala Phe Asp Ala
110 25 30
111
112 Thr Ile Ser Ile Lys Ser Tyr Pro Asp Lys Lys Phe Ser Tyr
113 35 40 45
114
115 Ser Ser Gly His Val His Leu Ser Ser Glu Asn Lys Phe Gln
116 50 55 60
117
118 Asn Ser Ala Ile Leu Thr Ile Gln Pro Lys Gln Leu Pro Gly
119 65 70 75
120
121 Gly Gln Asn Pro Val Ser Tyr Val Tyr Leu Glu Val Val Ser
122 80 85 90
123
124 Lys His Phe Ser Lys Ser Lys Arg Met Pro Ile Thr Tyr Asp
125 95 100
126
127 Asn Gly Phe Leu Phe Ile His Thr Asp Lys Pro Val Tyr Thr
128 105 110 115
129
130 Pro Asp Gln Ser Val Lys Val Arg Val Tyr Ser Leu Asn Asp
131 120 125 130
132
133 Asp Leu Lys Pro Ala Lys Arg Glu Thr Val Leu Thr Phe Ile
134 135 140 145
135
136 Asp Pro Glu Gly Ser Glu Val Asp Met Val Glu Glu Ile Asp
137 150 155 160
138
139 His Ile Gly Ile Ile Ser Phe Pro Asp Phe Lys Ile Pro Ser
140 165 170
141
142 Asn Pro Arg Tyr Gly Met Trp Thr Ile Lys Ala Lys Tyr Lys
143 175 180 185
144
145 Glu Asp Phe Ser Thr Thr Gly Thr Ala Tyr Phe Glu Val Lys
146 - 190 195 200
147
148 Glu Tyr Val Leu Pro His Phe Ser Val Ser Ile Glu Pro Glu
149 205 210 215
150
151 Tyr Asn Phe Ile Gly Tyr Lys Asn Phe Lys Asn Phe Glu Ile
152 220 225 230

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153
154 Thr Ile Lys Ala Arg Tyr Phe Tyr Asn Lys Val Val Thr Glu
155 235 240
156
157 Ala Asp Val Tyr Ile Thr Phe Gly Ile Arg Glu Asp Leu Lys
158 245 250 255
159
160 Asp Asp Gln Lys Glu Met Met Gln Thr Ala Met Gln Asn Thr
161 260 265 270
162
163 Met Leu Ile Asn Gly Ile Ala Gln Val Thr Phe Asp Ser Glu
164 275 280 285
165
166 Thr Ala Val Lys Glu Leu Ser Tyr Tyr Ser Leu Glu Asp Leu
167 290 295 300
168
169 Asn Asn Lys Tyr Leu Tyr Ile Ala Val Thr Val Ile Glu Ser
170 305 310
171
172 Thr Gly Gly Phe Ser Glu Glu Ala Glu Ile Pro Gly Ile Lys
173 315 320 325
174
175 Tyr Val Leu Ser Pro Tyr Lys Leu Asn Leu Val Ala Thr Pro
176 330 335 340
177
178 Leu Phe Leu Lys Pro Gly Ile Pro Tyr Pro Ile Lys Val Gln
179 345 350 355
180
181 Val Lys Asp Ser Leu Asp Gln Leu Val Gly Gly Val Pro Val
182 360 365 370
183
184 Ile Leu Asn Ala Gln Thr Ile Asp Val Asn Gln Glu Thr Ser
185 375 380
186
187 Asp Leu Asp Pro Ser Lys Ser Val Thr Arg Val Asp Asp Gly
188 385 390 395
189
190 Val Ala Ser Phe Val Leu Asn Leu Pro Ser Gly Val Thr Val
191 400 405 410
192
193 Leu Glu Phe Asn Val Lys Thr Asp Ala Pro Asp Leu Pro Glu
194 415 420 425
195
196 Glu Asn Gln Ala Arg Glu Gly Tyr Arg Ala Ile Ala Tyr Ser
197 430 435 440
198
199 Ser Leu Ser Gln Ser Tyr Leu Tyr Ile Asp Trp Thr Asp Asn
200 445 450
201
202 His Lys Ala Leu Leu Val Gly Glu His Leu Asn Ile Ile Val
203 455 460 465
204
205 Thr Pro Lys Ser Pro Tyr Ile Asp Lys Ile Thr His Tyr Asn

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206 470 475 480
207
208 Tyr Leu Ile Leu Ser Lys Gly Lys Ile Ile His Phe Gly Thr
209 485 490 495
210
211 Arg Glu Lys Phe Ser Asp Ala Ser Tyr Gln Ser Ile Asn Ile
212 500 505 510
213
214 Pro Val Thr Gln Asn Met Val Pro Ser Ser Arg Leu Leu Val
215 515 520
216
217 Tyr Tyr Ile Val Thr Gly Glu Gln Thr Ala Glu Leu Val Ser
218 525 530 535
219
220 Asp Ser Val Trp Leu Asn Ile Glu Glu Lys Cys Gly Asn Gln
221 540 545 550
222
223 Leu Gln Val His Leu Ser Pro Asp Ala Asp Ala Tyr Ser Pro
224 555 560 565
225
226 Gly Gln Thr Val Ser Leu Asn Met Ala Thr Gly Met Asp Ser
227 570 575 580
228
229 Trp Val Ala Leu Ala Ala Val Asp Ser Ala Val Tyr Gly Val
230 585 590
231
232 Gln Arg Gly Ala Lys Lys Pro Leu Glu Arg Val Phe Gln Phe
233 595 600 605
234
235 Leu Glu Lys Ser Asp Leu Gly Cys Gly Ala Gly Gly Leu
236 610 615 620
237
238 Asn Asn Ala Asn Val Phe His Leu Ala Gly Leu Thr Phe Leu
239 625 630 635
240
241 Thr Asn Ala Asn Ala Asp Asp Ser Gln Glu Asn Asp Glu Pro
242 640 645 650
243
244 Cys Lys Glu Ile Leu Arg Pro Arg Arg Thr Leu Gln Lys Lys
245 655 660
246
247 Ile Glu Glu Ile Ala Ala Lys Tyr Lys His Ser Val Val Lys
248 665 670 675
249
250 Lys Cys Cys Tyr Asp Gly Ala Cys Val Asn Asn Asp Glu Thr
251 680 685 690
252
253 Cys Glu Gln Arg Ala Ala Arg Ile Ser Leu Gly Pro Arg Cys
254 695 700 705
255
256 Ile Lys Ala Phe Thr Glu Cys Cys Val Val Ala Ser Gln Leu
257 710 715 720
258

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SEQUENCE VERIFICATION REPORT
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Original Text